|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Table S6. Annotation of genes with the correlation coefficient with 13 kDa prolamin ≥|0.7| | | | | | | |
| Gene ID | Name | Description | | | BINcode | | | Function |
| ENSRNA049445376 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049445384 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049445795 | tRNA-Gln | tRNA-Gln for anticodon CUG | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049446836 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049447201 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049447972 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049448151 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049449035 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049449070 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049449267 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049449660 | tRNA-Trp | tRNA-Trp for anticodon CCA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| ENSRNA049464941 | snoR86 | Small nucleolar RNA snoR86 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049464972 | snoR86 | Small nucleolar RNA snoR86 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049464985 | snoR86 | Small nucleolar RNA snoR86 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049465003 | snoZ279\_R105\_R108 | Small nucleolar RNA Z279/snoR105/snoR108 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049465125 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049465309 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049465332 | U54 | Small nucleolar RNA U54 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049465347 | U54 | Small nucleolar RNA U54 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049465412 | snoR60 | Small nucleolar RNA snoR60 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049465951 | snoZ169 | Small nucleolar RNA Z169 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049466017 | snoZ168 | Small nucleolar RNA Z168/Z174 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049466121 | snoZ168 | Small nucleolar RNA Z168/Z174 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049466137 | snoZ163 | Small nucleolar RNA Z163/Z177 family | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049466338 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049467117 | mir-166 | mir-166 microRNA precursor | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049467377 | U5 | U5 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049467441 | U2 | U2 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049467463 | U2 | U2 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049467714 | snoR134 | small nucleolar RNA snoR134 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049467734 | snoZ278 | Small nucleolar RNA Z278 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049467742 | MIR1428 | microRNA MIR1428 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049467928 | U1 | U1 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468027 | SNORD36 | Small nucleolar RNA SNORD36 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468126 | snoR44\_J54 | Small nucleolar RNA R44/J54/Z268 family | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468154 | U4 | U4 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468200 | U1 | U1 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468231 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049468241 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049468277 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049468467 | MIR820 | microRNA MIR820 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468702 | U6 | U6 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468709 | snoR134 | small nucleolar RNA snoR134 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468722 | snoZ223 | Small nucleolar RNA Z223 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468767 | MIR820 | microRNA MIR820 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049468908 | snoU31b | Small nucleolar RNA U31b | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049469003 | snoR44\_J54 | Small nucleolar RNA R44/J54/Z268 family | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049469217 | U1 | U1 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049469734 | snoZ279\_R105\_R108 | Small nucleolar RNA Z279/snoR105/snoR108 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049469812 | U2 | U2 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049470113 | snoR117 | small nucleolar RNA snoR117 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049470180 | U5 | U5 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049470195 | MIR171\_1 | microRNA MIR171\_1 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049470386 | snoZ278 | Small nucleolar RNA Z278 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049470425 | U54 | Small nucleolar RNA U54 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049470806 | U1 | U1 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049470973 | U12 | U12 minor spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049470992 | snoZ221\_snoR21b | Small nucleolar RNA Z221/R21b | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049471032 | SNORD14 | Small nucleolar RNA SNORD14 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049471043 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049471090 | 5\_8S\_rRNA | 5.8S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049471102 | SSU\_rRNA\_eukarya | Eukaryotic small subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049471325 | snoZ102\_R77 | Small nucleolar RNA Z102/R77 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049471381 | MIR159 | microRNA MIR159 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049471535 | RNase\_MRP | RNase MRP | | | 35 | 35 | | Unknown |
| ENSRNA049471546 | U4 | U4 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049471602 | Plant\_SRP | Plant signal recognition particle RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049471778 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049471985 | snoZ118 | Small nucleolar RNA Z118/Z121/Z120 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472003 | snoZ118 | Small nucleolar RNA Z118/Z121/Z120 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472018 | snoR11 | Small nucleolar RNA R11/Z151 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472073 | snoZ118 | Small nucleolar RNA Z118/Z121/Z120 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472089 | snoZ152 | Small nucleolar RNA Z152/R70/R12/ | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472132 | snoZ199 | Small nucleolar RNA Z199 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472195 | snoZ118 | Small nucleolar RNA Z118/Z121/Z120 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472208 | snoZ118 | Small nucleolar RNA Z118/Z121/Z120 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472231 | snoZ118 | Small nucleolar RNA Z118/Z121/Z120 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472320 | U2 | U2 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472337 | U2 | U2 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472543 | MIR1428 | microRNA MIR1428 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472690 | snoZ105 | Small nucleolar RNA Z105 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472907 | SNORD14 | Small nucleolar RNA SNORD14 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049472947 | SNORD24 | Small nucleolar RNA SNORD24 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473120 | snoU31b | Small nucleolar RNA U31b | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473128 | SNORD14 | Small nucleolar RNA SNORD14 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473164 | SNORD14 | Small nucleolar RNA SNORD14 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473172 | SNORD14 | Small nucleolar RNA SNORD14 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473180 | SNORD14 | Small nucleolar RNA SNORD14 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473223 | SNORD14 | Small nucleolar RNA SNORD14 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473260 | U1 | U1 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473335 | SSU\_rRNA\_eukarya | Eukaryotic small subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049473437 | Plant\_U3 | Plant small nucleolar RNA U3 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473610 | SNORD25 | Small nucleolar RNA SNORD25 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473620 | SNORD25 | Small nucleolar RNA SNORD25 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473627 | SNORD25 | Small nucleolar RNA SNORD25 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473842 | snoZ266 | Small nucleolar RNA Z266 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473876 | snoZ103 | Small nucleolar RNA Z103 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473879 | snoZ103 | Small nucleolar RNA Z103 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473887 | snoZ103 | Small nucleolar RNA Z103 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473899 | snoZ223 | Small nucleolar RNA Z223 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473908 | snoR134 | small nucleolar RNA snoR134 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049473918 | U1 | U1 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049474010 | MIR171\_1 | microRNA MIR171\_1 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049474050 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049474061 | U5 | U5 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049474711 | 5S\_rRNA | 5S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049475361 | 5S\_rRNA | 5S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049475575 | snoZ43 | Small nucleolar RNA Z43 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049475592 | U5 | U5 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049475677 | SSU\_rRNA\_eukarya | Eukaryotic small subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049475720 | U54 | Small nucleolar RNA U54 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049475757 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049475834 | U6 | U6 spliceosomal RNA | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049475930 | snoZ159 | Small nucleolar RNA Z159/U59 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049475944 | LSU\_rRNA\_eukarya | Eukaryotic large subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049475950 | snoR135 | small nucleolar RNA snoR135 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049476188 | snoZ242 | Small nucleolar RNA Z242 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049476209 | Plant\_U3 | Plant small nucleolar RNA U3 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049476293 | snoZ242 | Small nucleolar RNA Z242 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049476335 | snosnR60\_Z15 | Small nucleolar RNA snR60/Z15/Z230/Z193/J17 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049476340 | MIR171\_1 | microRNA MIR171\_1 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049476404 | snoZ266 | Small nucleolar RNA Z266 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049476411 | snoZ266 | Small nucleolar RNA Z266 | | | 27 | 27.1 | | RNA.processing |
| ENSRNA049476430 | SSU\_rRNA\_eukarya | Eukaryotic small subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476437 | SSU\_rRNA\_eukarya | Eukaryotic small subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476444 | SSU\_rRNA\_eukarya | Eukaryotic small subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476447 | SSU\_rRNA\_eukarya | Eukaryotic small subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476452 | SSU\_rRNA\_eukarya | Eukaryotic small subunit ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476493 | 5\_8S\_rRNA | 5.8S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476498 | 5\_8S\_rRNA | 5.8S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476502 | 5\_8S\_rRNA | 5.8S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476508 | 5\_8S\_rRNA | 5.8S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA049476514 | 5\_8S\_rRNA | 5.8S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA050013642 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013643 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013644 | 5S\_rRNA | 5S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA050013645 | 5S\_rRNA | 5S ribosomal RNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| ENSRNA050013646 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013647 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013650 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013661 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013662 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013664 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013665 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013666 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013667 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013668 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| ENSRNA050013672 | Intron\_gpII | Group II catalytic intron | | | 27 | 27.1 | | RNA.processing |
| EPlORYSAT000373608 | rrn26 | rRNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| EPlORYSAT000373610 | pseudo-trnV | tRNA pseudogene | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373611 | rrn5 | rRNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| EPlORYSAT000373615 | trnR | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373619 | trnD | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373647 | rrn18 | rRNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| EPlORYSAT000373657 | trnS | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373785 | tRNA-Ser (UGA) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373795 | tRNA-Thr (GGU) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373805 | tRNA-Val (UAC) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373810 | tRNA-Tyr (GUA) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373811 | rRNA | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373814 | tRNA-Ser (GCU) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373829 | rRNA | rRNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| EPlORYSAT000373834 | rRNA | rRNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| EPlORYSAT000373835 | tRNA-Arg (UCU) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373839 | rRNA | rRNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| EPlORYSAT000373840 | tRNA-Asp (GUC) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373848 | tRNA-His (GUG) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373849 | rRNA | rRNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| EPlORYSAT000373852 | rRNA | rRNA | | | 29 | 29.2.6 | | Protein synthesis-ribosomal RNA |
| EPlORYSAT000373862 | tRNA-Ile (GAU) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373867 | tRNA-Pro (UGG) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| EPlORYSAT000373872 | tRNA-Ile (GAU) | tRNA | | | 29 | 29.2.7 | | Protein synthesis\_transfer RNA |
| gene-atp1 |  | ATP synthase subunit alpha | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-atp6 |  | ATP synthase subunit a | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-atp9 |  | ATP synthase subunit 9, mitochondrial | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-cox1 |  | unknown | | | 35 | 35 | | Unknown |
| gene-cox2 |  | Cytochrome c oxidase subunit 2 | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-cox3 |  | Cytochrome c oxidase subunit 3 | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-nad2 |  | unknown | | | 35 | 35 | | Unknown |
| gene-nad4L |  | NADH dehydrogenase subunit 4L | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-nad5 |  | unknown | | | 35 | 35 | | Unknown |
| gene-nad6 |  | NADH-ubiquinone oxidoreductase chain 6 | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-nad7 |  | NAD(P)H dehydrogenase subunit H | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-nad9 |  | NADH dehydrogenase subunit 9 | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-orf25 |  | ATP synthase protein MI25 | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-orfB |  | H(+)-transporting two-sector ATPase | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| gene-petE |  | Cytochrome b6-f complex subunit 5 | | | 1 | 1 | | Photosyntheisis |
| gene-psbK |  | Chloroplast PSII K protein | | | 1 | 1 | | Photosyntheisis |
| gene-rpl36 |  | Large ribosomal subunit protein bL36c | | | 29 | 29.2.1 | | Protein.synthesis\_ribosomal protein |
| gene-rps1 |  | Ribosomal protein S1 | | | 29 | 29.2.1 | | Protein.synthesis\_ribosomal protein |
| Os01g0106400 |  | Similar to Isoflavone reductase homolog IRL (EC 1.3.1.-) | | | 16 | 16.8.5.1 | | Secondary metabolism.flavonoids.isoflavones.isoflavone reductase |
| Os01g0127600 |  | Similar to Bowman-Birk type proteinase inhibitor D-II precursor (IV) | | | 35 | 35.2 | | Unknown |
| Os01g0148000 |  | E3 ubiquitin-protein ligase | | | 29 | 29.5.11 | | Protein degradation ubiquitin |
| Os01g0179600 | OsUGT75K1 | UDP-glucuronosyl/UDP-glucosyltransferase family protein | | | 26 | 26.2 | | Misc.UDP glucosyl and glucoronyl transferases |
| Os01g0209500 |  | Zinc finger%2C RING-type domain containing protein | | | 27 | 27.3.67 | | RNA.regulation of transcription.putative transcription regulator |
| Os01g0209566 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0212000 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0221400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os01g0237200 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0252300 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os01g0262500 |  | TRAM/LAG1/CLN8 homology domain domain containing protein | | | 35 | 35.2 | | Unknown |
| Os01g0281301 |  | Protein of unknown function DUF1645 domain containing protein | | | 35 | 35.2 | | Unknown |
| Os01g0287400 |  | Similar to Hydrophobic protein LTI6A (Low temperature-induced protein 6A) | | | 35 | 35 | | Unknown |
| Os01g0288700 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os01g0303000 |  | Similar to CP12 (Fragment) | | | 1 | 1.3 | | Photosyntheisis |
| Os01g0323775 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0331500 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0361700 |  | Conserved hypothetical protein | | | 11 | 11.7 | | Lipid metabolism.unassigned |
| Os01g0371200 | OsGSTF1 | Similar to Glutathione-S-transferase 19E50 | | | 26 | 26.9 | | misc.glutathione S transferases |
| Os01g0374000 | OsGSTF12 | Similar to Glutathione S-transferase I (EC 2.5.1.18) (GST-I) (GST-29) (GST class- phi) | | | 26 | 26.9 | | misc.glutathione S transferases |
| Os01g0374100 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0384450 |  | Similar to H0124E07.4 protein | | | 35 | 35.2 | | Unknown |
| Os01g0387566 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0392600 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os01g0444100 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os01g0524251 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0541800 | OsSWEET2a | MtN3 and saliva related transmembrane protein family protein | | | 33 | 33.99 | | Development.unspecified |
| Os01g0550250 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0559550 |  | Non-protein coding transcript | | | 33 | 33.99 | | Development.unspecified |
| Os01g0576050 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os01g0579900 |  | Esterase/lipase/thioesterase domain containing protein | | | 35 | 35.2 | | Unknown |
| Os01g0586900 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0593700 | OsSultr3 | Sulphate transporter domain containing protein | | | 34 | 34.6 | | Transport sulphate |
| Os01g0594500 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os01g0606900 | OsDjC10 | Heat shock protein DnaJ%2C N-terminal domain containing protein | | | 20 | 20.2.1 | | Stress.abiotic.heat |
| Os01g0626350 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0634600 | OsPME4 | Pectin lyase fold/virulence factor domain containing protein | | | 10 | 10.8.1 | | Cell wall.pectin\*esterases.PME |
| Os01g0639900 | BETACA1 | beta-carbonic anhydrase (EC:4.2.1.1)%2C Carbon assimilation%2C CO<sub>2</sub>-mediated stomatal pore respons | | | 8 | 8.3 | | TCA / org. transformation |
| Os01g0652650 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0656600 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os01g0667550 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os01g0678900 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0682001 |  | Similar to NADH dependent Glutamate Synthase | | | 12 | 12.2.1 | | N-metabolism.ammonia metabolism.glutamate synthase |
| Os01g0687500 |  | Methionine tRNA Formyltransferase-like domain containing protein | | | 13 | 13.2.3.4 | | amino acid metabolism.degradation.aspartate family.methionine |
| Os01g0692000 | OsGSTU40 | Similar to Glutathione S-transferase GSTU6 | | | 26 | 26.9 | | misc.glutathione S transferases |
| Os01g0702450 |  | Similar to Chaperone protein dnaJ 10 | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| Os01g0702900 |  | Similar to Sucrose-phosphate synthase (EC 2.4.1.14) | | | 27 | 27.1 | | RNA.processing |
| Os01g0725000 |  | Similar to H0402C08.3 protein | | | 35 | 35.2 | | Unknown |
| Os01g0725900 |  | Similar to arabinogalactan protein | | | 35 | 35.2 | | Unknown |
| Os01g0733200 | OsHsfC1b | Similar to Heat shock transcription factor 29 (Fragment) | | | 27 | 27.3.23 | | RNA.regulation of transcription.HSF,Heat-shock transcription factor family |
| Os01g0734150 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os01g0734200 | rbohA | Similar to respiratory burst oxidase protein B | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| Os01g0737200 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0741250 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0741900 | IAA6 | Auxin-responsive protein%2C Drought tolerance%2C Control of tiller outgrowt | | | 17 | 17.2.3 | | Hormone metabolism.auxin.induced-regulated-responsive-activated |
| Os01g0745850 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0748150 | OsENODL1 | Cupredoxin domain containing protein | | | 26 | 26.19 | | misc.plastocyanin-like |
| Os01g0750300 | OsCesA4 | Similar to Cellulose synthase (Fragment) | | | 10 | 10.2.1 | | Cell wall.cellulose synthesis.cellulose synthase |
| Os01g0760701 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os01g0761400 |  | TGF-beta receptor%2C type I/II extracellular region family protein | | | 34 | 34.13 | | transport.peptides and oligopeptides |
| Os01g0778500 |  | Similar to predicted protein | | | 35 | 35.2 | | Unknown |
| Os01g0787600 | OsPOP4 | Similar to Salicylic acid-binding protein 2 | | | 26 | 26.8 | | Misc.nitrilases, \*nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases |
| Os01g0794400 |  | Thioredoxin domain 2 containing protein | | | 35 | 35.2 | | Unknown |
| Os01g0798200 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0805900 | OsTUB4 | Tubulin beta-2 chain (Beta-2 tubulin) | | | 31 | 31.1 | | Cell organisation |
| Os01g0812100 |  | Similar to NHL25 | | | 33 | 33.2 | | Development.late embryogenesis abundant |
| Os01g0819300 | OsNTMC2T1.3 | Similar to calcium lipid binding protein-like | | | 30 | 30.3 | | Signalling.calcium |
| Os01g0825800 | OsATL7 | Amino acid transporter%2C transmembrane domain containing protein | | | 34 | 34.3 | | Transport.amino acids |
| Os01g0829400 | OsGRL2 | Thioredoxin fold domain containing protein | | | 21 | 21.4 | | redox.glutaredoxins |
| Os01g0829600 |  | Protein of unknown function DUF688 domain containing protein | | | 35 | 35.2 | | Unknown |
| Os01g0840100 | OsMed37\_1 | Heat shock protein Hsp70 family protein | | | 20 | 20.2.1 | | Stress |
| Os01g0846700 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0846800 |  | Regulator of chromosome condensation%2C RCC1 domain containing protein | | | 31 | 31.2 | | Cell division |
| Os01g0860601 |  | Similar to Ferredoxin%2C root R-B1 | | | 1 | 1.1.5.2 | | Photosyntheisis |
| Os01g0872100 |  | TGF-beta receptor%2C type I/II extracellular region family protein | | | 34 | 34.13 | | Transport.peptides and oligopeptides |
| Os01g0880300 | OsPME7 | Similar to Pectin methylesterase-like protein | | | 10 | 10.8.1 | | Cell wall.pectin\*esterases.PME |
| Os01g0899387 |  | Conserved hypothetical protein | | | 3 | 3.6 | | minor CHO metabolism |
| Os01g0909150 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os01g0915300 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0915401 |  | Proteinase inhibitor I25%2C cystatin domain containing protein | | | 35 | 35.2 | | Unknown |
| Os01g0926300 |  | Similar to Transaldolase (EC 2.2.1.2) | | | 7 | 7.2.2 | | OPP |
| Os01g0937100 |  | Similar to Xylanase inhibitor precursor (Xylanase inhibitor TAXI-I) | | | 29 | 29.5.4 | | Protein.degradation.aspartate protease |
| Os01g0939901 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os01g0958200 |  | Curculin-like (mannose-binding) lectin domain containing protein | | | 29 | 29.4 | | Protein.postranslational modification |
| Os01g0971800 | OsPCL1 | Transcription factor with a GARP DNA-binding domain%2C Photoperiodic control of flowering time%2C Clock associated-componen | | | 27 | 27.3.20 | | RNA.regulation of transcription.G2-like transcription factor family, GARP |
| Os01g0974400 | XBOS31 | Zinc finger%2C RING/FYVE/PHD-type domain containing protein | | | 31 | 31.1 | | Cell organisation |
| Os01g0974600 |  | Similar to Histone H2A | | | 35 | 35 | | Unknown |
| Os02g0102900 | OsCPn60beta2 | Similar to RuBisCO subunit binding-protein beta subunit%2C chloroplast (60 kDa chaperonin beta subunit) (CPN-60 beta) (Fragment) | | | 29 | 29.6 | | Protein.folding |
| Os02g0106966 |  | Similar to emb1507 (embryo defective 1507)%3B ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding / nucleoside-triphosphatase/ nucleotide binding | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| Os02g0115950 |  | Glutamate dehydrogenase%2C NAD-specific domain containing protein | | | 9 | 9 | | Mitochondrial electron transport / ATP synthesis |
| Os02g0129000 |  | Hypothetical conserved gene | | | 4 | 4.1.6 | | Protein.postranslational modification.kinase.receptor like cytoplasmatic kinase X |
| Os02g0129800 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os02g0134200 | OsSGL | DUF1645 family protein%2C Regulation of stress-tolerance and grain lengt | | | 20 | 20 | | Stress |
| Os02g0152800 |  | RNA polymerase Rpb1%2C domain 1 containing protein | | | 27 | 27.2 | | RNA.transcription |
| Os02g0175950 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os02g0187300 |  | Similar to predicted protein | | | 35 | 35.2 | | Unknown |
| Os02g0189400 |  | Defence response%2C Rin4 domain containing protein | | | 30 | 30.1 | | Signalling.in sugar and nutrient physiology |
| Os02g0191300 | OsATL6 | Similar to Amino acid transporter-like protein | | | 34 | 34.3 | | Transport.amino acids |
| Os02g0191700 |  | EF-HAND 2 domain containing protein | | | 30 | 30.3 | | Signalling.calcium |
| Os02g0192250 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os02g0193967 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os02g0226350 |  | Non-protein coding transcript | | | 34 | 34.9 | | Transport.metabolite transporters at the mitochondrial membrane |
| Os02g0227100 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os02g0244450 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os02g0257400 |  | Non-protein coding transcript | | | 26 | 26.23 | | Misc.rhodanese |
| Os02g0301450 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os02g0322251 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os02g0322400 |  | Similar to NPKL2 (Fragment) | | | 29 | 29.4 | | Protein.postranslational modification |
| Os02g0452700 |  | Hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os02g0514500 |  | Similar to Glycerophosphoryl diester phosphodisterase (Fragment) | | | 11 | 11.9.3.3 | | Lipid metabolism.lipid degradation.lysophospholipases.glycerophosphodiester phosphodiesterase |
| Os02g0519700 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os02g0527200 |  | Similar to OSIGBa0142C11.2 protein | | | 35 | 35.2 | | Unknown |
| Os02g0533200 |  | SOUL haem-binding protein domain containing protein | | | 21 | 21.3 | | redox.heme |
| Os02g0541300 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os02g0549850 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os02g0553802 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os02g0563000 | OsKMD3 | Hypothetical conserved gene | | | 29 | 29.5.11.4.3.2 | | Protein.degradation.ubiquitin.E3.SCF.FBOX |
| Os02g0580500 |  | Similar to Prohibitin | | | 9 | 9.1.1 | | Mitochondrial electron transport / ATP synthesis.NADH-DH.complex I |
| Os02g0586900 | OsEnS-40 | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os02g0594232 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os02g0594700 |  | Similar to Non-phototropic hypocotyl 3 | | | 30 | 30.11 | | Signalling.light |
| Os02g0604000 | OsGELP38 | Similar to alpha-L-fucosidase 2 | | | 26 | 26.28 | | Misc.GDSL-motif lipase |
| Os02g0629000 |  | Protein of unknown function DUF584 family protein | | | 35 | 35.2 | | Unknown |
| Os02g0630250 |  | Similar to predicted protein | | | 35 | 35.2 | | Unknown |
| Os02g0635400 |  | Non-protein coding transcript | | | 35 | 35.2 | | Unknown |
| Os02g0653300 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os02g0666250 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os02g0670500 | OsRALF-8 | Rapid ALkalinization Factor family protein | | | 30 | 30.8 | | Signalling.misc |
| Os02g0685200 | OsMyb1R | MYB transcription factor%2C Transcriptional activator in mediating stress and rhythm responsivegene expressio | | | 27 | 27.3.26 | | RNA.regulation of transcription.MYB-related transcription factor family |
| Os02g0688800 |  | Non-protein coding transcript | | | 29 | 29.5.11.4.2 | | Protein.degradation.ubiquitin.E3.RING |
| Os02g0693500 |  | Similar to OSIGBa0142I02-OSIGBa0101B20.17 protein | | | 35 | 35.2 | | Unknown |
| Os02g0708500 |  | Conserved hypothetical protein | | | 27 | 27.3.11 | | RNA.regulation of transcription.C2H2 zinc finger family |
| Os02g0722300 |  | Nonaspanin (TM9SF) family protein | | | 28 | 28.99 | | DNA.unspecified |
| Os02g0728850 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os02g0730075 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os02g0732800 | OsGELP43 | Similar to Anther-specific proline-rich protein APG | | | 26 | 26.28 | | Misc.GDSL-motif lipase |
| Os02g0738600 | OsGH9B8 | Similar to CEL5%3DCELLULASE 5 (Fragment) | | | 26 | 26.3.4 | | Misc.gluco-, galacto- and mannosidases.endoglucanase |
| Os02g0761500 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os02g0772000 |  | Similar to global transcription factor group | | | 27 | 27.3.52 | | RNA.regulation of transcription.Global transcription factor group |
| Os02g0783650 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os02g0783700 |  | Similar to Lysine ketoglutarate reductase/saccharopine dehydrogenase | | | 13 | 13.2.3.5 | | Amino acid metabolism.degradation.aspartate family.lysine |
| Os02g0801255 |  | Similar to cDNA clone:J013118P06%2C full insert sequence | | | 35 | 35.2 | | Unknown |
| Os02g0822050 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os03g0111200 | OsREM1.3 | Similar to Remorin | | | 27 | 27.3.99 | | RNA.regulation of transcription.unclassified |
| Os03g0111400 |  | Heavy metal transport/detoxification protein domain containing protein | | | 35 | 35.2 | | Unknown |
| Os03g0112900 | OsF5HL2 | Similar to Aldehyde 5-hydroxylase | | | 26 | 26.1 | | Misc.misc2 |
| Os03g0117100 | PEX11-1 | Peroxisomal protein%2C Response to salt and low nitrogen stresse | | | 29 | 29.3.5 | | Protein.targeting.peroxisomes |
| Os03g0126700 |  | Similar to Barley stem rust resistance protein | | | 28 | 28.2 | | DNA.repair |
| Os03g0128600 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0133500 | OsACS | Similar to Adenosine monophosphate binding protein 1 AMPBP1 | | | 11 | 11.1.8 | | Lipid metabolism.FA synthesis and FA elongation.acyl coa ligase |
| Os03g0133850 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os03g0137250 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os03g0145751 |  | Hypothetical genes | | | 35 | 35 | | Unknown |
| Os03g0146800 | OsIPS1 | Non-protein coding transcript | | | 35 | 35.2 | | Unknown |
| Os03g0180100 |  | Protein of unknown function DUF1677%2C plant domain containing protein | | | 35 | 35.2 | | Unknown |
| Os03g0192750 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os03g0204500 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0226200 | HB2 | Non-symbiotic hemoglobin 2 (rHb2 | | | 21 | 21.3 | | redox.heme |
| Os03g0232400 |  | Phytosulfokine family protein | | | 35 | 35.2 | | Unknown |
| Os03g0237500 |  | Similar to predicted protein | | | 35 | 35.2 | | Unknown |
| Os03g0245800 | OsHSP26 | Similar to Heat shock protein 26 | | | 20 | 20.2.1 | | Stress |
| Os03g0254250 |  | Non-protein coding transcript | | | 35 | 35.2 | | Unknown |
| Os03g0262200 |  | Similar to predicted protein | | | 29 | 29.4 | | Protein.postranslational modification |
| Os03g0265900 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0266100 |  | Zinc finger%2C LIM-type domain containing protein | | | 33 | 33.99 | | Development.unspecified |
| Os03g0267100 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os03g0267200 | OsHsp17.7 | Low molecular mass heat shock protein Oshsp17.7 | | | 20 | 20.2.1 | | Stress |
| Os03g0276500 | OsHsp71.1 | Similar to Heat shock protein 70 | | | 20 | 20.2.1 | | Stress |
| Os03g0290900 | OsTBL18 | Protein of unknown function DUF231%2C plant domain containing protein | | | 35 | 35.2 | | Unknown |
| Os03g0293000 | OsERdj3A | Similar to DnaJ domain containing protein%2C expressed | | | 20 | 20.2.1 | | Stress |
| Os03g0299700 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0306900 |  | Haem oxygenase-like%2C multi-helical domain containing protein | | | 35 | 35.2 | | Unknown |
| Os03g0351700 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0369100 | OsLTPL36 | Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein | | | 11 | 11.6 | | Lipid metabolism.lipid transfer proteins etc |
| Os03g0379650 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os03g0381300 |  | CS domain domain containing protein | | | 35 | 35.2 | | Unknown |
| Os03g0388432 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os03g0407050 |  | Hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0409400 |  | Similar to mps one binder kinase activator-like 1A | | | 27 | 27.3.99 | | RNA.regulation of transcription.unclassified |
| Os03g0432277 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os03g0441050 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os03g0567100 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0586500 |  | Similar to chloroplast post-illumination chlorophyll fluorescence increase protein | | | 1 | 1.1.40 | | Photosyntheisis |
| Os03g0618366 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os03g0629800 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0643611 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os03g0648450 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os03g0663800 | OsEnS-51 | Globulin 1 (Fragment) | | | 33 | 33.1 | | Development.storage proteins |
| Os03g0679700 | OsTHIC | Similar to Thiamine biosynthesis protein thiC | | | 18 | 18.2 | | Co-factor and vitamine metabolism.thiamine |
| Os03g0682200 | OsAGO12 | Similar to Protein argonaute 12 | | | 33 | 33.99 | | Development.unspecified |
| Os03g0721900 |  | Similar to Histone H2A | | | 28 | 28.1.3 | | DNA.synthesis/chromatin structure.histone |
| Os03g0722500 |  | Glycoside hydrolase%2C family 17 protein | | | 26 | 26.4.1 | | Misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase |
| Os03g0726300 | OsOSCA2.3 | Protein of unknown function DUF221 domain containing protein | | | 20 | 20.2.3 | | Stress.abiotic.drought/salt |
| Os03g0738350 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os03g0745000 | HSfA2a | Similar to Heat stress transcription factor A-2a | | | 27 | 27.2 | | RNA.transcription |
| Os03g0764250 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os03g0764300 | OsMAPKKK18 | Serine/threonine protein kinase domain containing protein | | | 29 | 29.4 | | Protein.postranslational modification |
| Os03g0765400 |  | Similar to nucleoporin p58/p45 | | | 29 | 29.3.1 | | Protein.targeting.nucleus |
| Os03g0768450 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os03g0776900 | OsDjC35 | Similar to mitochondrial import inner membrane translocase subunit TIM14 | | | 20 | 20.2.1 | | Stress |
| Os03g0794000 | OsLTPG9 | Plant lipid transfer protein/Par allergen family protein | | | 11 | 11.6 | | Lipid metabolism.lipid transfer proteins etc |
| Os03g0797400 | OsIGL | Similar to Indole-3-glycerol phosphate lyase | | | 13 | 13.1.6.5.5 | | Amino acid metabolism.synthesis.aromatic aa.tryptophan.tryptophan synthase |
| Os03g0808500 | OsLTP1.3 | Plant lipid transfer protein/Par allergen family protein | | | 11 | 11.6 | | Lipid metabolism.lipid transfer proteins etc |
| Os03g0810700 |  | Similar to Mitochondrial Rho GTPase | | | 30 | 30.5 | | Signalling.G-proteins |
| Os03g0821275 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os03g0826800 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os03g0828500 |  | Similar to (1-4)-beta-mannan endohydrolase precursor (EC 3.2.1.78) | | | 10 | 10.6.2 | | Cell wall.degradation.mannan-xylose-arabinose-fucose |
| Os03g0832200 | CRT | Similar to Calcium-binding protein precursor (Calreticulin) | | | 30 | 30.3 | | Signalling.calcium |
| Os03g0844301 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os04g0103601 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os04g0105050 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os04g0107900 | Hsp90 | Similar to Heat shock protein 82 | | | 20 | 20.2.1 | | Stress |
| Os04g0118450 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os04g0119300 |  | Similar to H0716A07.6 protein | | | 35 | 35.2 | | Unknown |
| Os04g0162500 |  | Zinc finger%2C C2H2-type domain containing protein | | | 27 | 27.3 | | RNA.regulation of transcription |
| Os04g0173800 |  | Lectin precursor (Agglutinin) | | | 20 | 20.1 | | Stress.biotic |
| Os04g0210700 |  | Similar to OSIGBa0114M03.3 protein | | | 1 | 1 | | Photosyntheisis |
| Os04g0223500 |  | Dimethylaniline monooxygenase%2C N-oxide-forming domain containing protein | | | 26 | 26.7 | | Misc.oxidases - copper, flavone etc. |
| Os04g0252850 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os04g0372775 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os04g0409200 | OsBEIIa |  | 2.1.2.3 |
| Os04g0412000 |  | Hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os04g0429087 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os04g0445100 |  | Similar to 22.7 kDa class IV heat shock protein precursor | | | 20 | 20.2.1 | | Stress |
| Os04g0445700 |  | Similar to OSIGBa0140O07.8 protein | | | 11 | 11.1.3 | | Lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase |
| Os04g0450900 |  | Protein kinase PKN/PRK1%2C effector domain containing protein | | | 29 | 29.4 | | Protein.postranslational modification |
| Os04g0479550 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os04g0481050 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os04g0481200 |  | Similar to H0510A06.2 protein | | | 26 | 26.3.5 | | Misc.gluco-, galacto- and mannosidases.glycosyl hydrolase family 5 |
| Os04g0483450 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os04g0485700 |  | Similar to Exonuclease | | | 35 | 35.2 | | Unknown |
| Os04g0502900 |  | EF-Hand type domain containing protein | | | 30 | 30.3 | | Signalling.calcium |
| Os04g0511200 | EFA27 | EFA27 for EF hand%2C abscisic acid%2C 27kD | | | 33 | 33.99 | | Development.unspecified |
| Os04g0522100 | DEFL12 | Similar to OSIGBa0131L05.12 protein | | | 35 | 35.2 | | Unknown |
| Os04g0526800 |  | GRAM domain containing protein | | | 17 | 17.1.3 | | Hormone metabolism.abscisic acid.induced-regulated-responsive-activated |
| Os04g0527000 |  | GRAM domain containing protein | | | 17 | 17.1.3 | | Hormone metabolism.abscisic acid.induced-regulated-responsive-activated |
| Os04g0528000 | OsEnS-71 | Similar to OSIGBa0115K01-H0319F09.15 protein | | | 35 | 35.2 | | Unknown |
| Os04g0533602 |  | Hypothetical genes | | | 35 | 35 | | Unknown |
| Os04g0538166 |  | Similar to Elongation factor G%2C chloroplastic | | | 29 | 29.2.4 | | Protein.synthesis.elongation |
| Os04g0552300 | CycU2 | Cyclin-related 2 domain containing protein | | | 31 | 31.3 | | Cell cycle |
| Os04g0560600 | CDPK12 | Calcium-dependent protein kinase%2C Salt-stress tolerance%2C Blast disease resistanc | | | 30 | 30.3 | | Signalling.calcium |
| Os04g0563350 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os04g0573700 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os04g0583900 | LHY | Similar to LHY protein | | | 27 | 27.3.26 | | RNA.regulation of transcription.MYB-related transcription factor family |
| Os04g0587200 |  | Similar to invertase inhibitor | | | 26 | 26.18 | | Misc.invertase/pectin methylesterase inhibitor family protein |
| Os04g0602250 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os04g0614300 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os04g0615200 |  | Hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os04g0616250 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os04g0617050 | OsSAUR21 | Similar to H0313F03.1 protein | | | 17 | 17.2.3 | | Hormone metabolism.auxin.induced-regulated-responsive-activated |
| Os04g0617500 |  | Similar to H0313F03.4 protein | | | 35 | 35 | | Unknown |
| Os04g0625850 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os04g0641101 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os04g0659800 | OsAAP7B | Similar to OSIGBa0132E09-OSIGBa0108L24.20 protein | | | 34 | 34.3 | | Transport.amino acids |
| Os04g0661250 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os04g0669900 | OsMTK2 | Similar to H0818H01.11 protein | | | 13 | 13.99 | | Amino acid metabolism.misc |
| Os04g0673300 | RR6 | A-type response regulator%2C Cytokinin signalin | | | 27 | 27.3.5 | | RNA.regulation of transcription.ARR |
| Os04g0674025 |  | Similar to H0403D02.10 protein | | | 35 | 35 | | Unknown |
| Os04g0675400 | OsDjC45 | Similar to Chaperone protein dnaJ | | | 20 | 20.2.1 | | Stress |
| Os04g0681600 |  | Protein of unknown function DUF580 family protein | | | 34 | 34.99 | | Transport.misc |
| Os04g0682100 |  | C2 calcium/lipid-binding region%2C CaLB domain containing protein | | | 35 | 35.2 | | Unknown |
| Os04g0682400 |  | Similar to H0124B04.13 protein | | | 27 | 27.1 | | RNA.processing |
| Os04g0684800 | OsUEV1D | Similar to CROC-1-like protein (Fragment) | | | 29 | 29.5.11.3 | | Protein.degradation.ubiquitin.E2 |
| Os05g0100100 |  | Similar to cDNA clone:006-204-G09%2C full insert sequence | | | 35 | 35.2 | | Unknown |
| Os05g0102700 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os05g0103400 |  | Protein of unknown function DUF3339 domain containing protein | | | 35 | 35.2 | | Unknown |
| Os05g0103800 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os05g0104700 | PGIP4 | Leucine-rich repeat (LRR) protein%2C Inhibitor of fungal polygalacturonase%2C Defence respons | | | 10 | 10.6.3 | | Cell wall.degradation.pectate lyases and polygalacturonases |
| Os05g0121725 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os05g0132601 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os05g0156900 | Chalk5 | Vacuolar H+-translocating pyrophosphatase%2C Regulation of grain chalkines | | | 34 | 34.3 | | Transport.amino acids |
| Os05g0167300 |  | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os05g0179950 |  | Similar to cDNA%2C clone: J100088D24%2C full insert sequence | | | 26 | 26.2 | | Misc.UDP glucosyl and glucoronyl transferases |
| Os05g0217000 | OsAGP23 | Protein of unknown function DUF1070 family protein | | | 35 | 35.2 | | Unknown |
| Os05g0228900 |  | Hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os05g0270500 | OsRPP14.1 | Similar to predicted protein | | | 18 | 18 | | Co-factor and vitamine metabolism |
| Os05g0328300 | OsOFP33 | Similar to OFP17 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 17) | | | 35 | 35.2 | | Unknown |
| Os05g0328333 | pro13b.5 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0328466 | pro13b.6 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0328901 | pro13b.9 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0329001 | pro13b.10 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0329100 | pro13b.11 | Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0329200 | pro13b.16 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0329300 | pro13b.12 | Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0329350 | pro13b.13 | Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0329400 | pro13b.14 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0329700 | pro13b.15 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0330150 | pro13b.17 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0330600 | pro13b.18 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0331366 | pro13b.19 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0331532 | pro13b.20 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0331800 | pro13b.21 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0331900 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os05g0332000 | pro13b.22 | Similar to Prolamin precursor | | | 33 | 33.1 | | Development.storage proteins |
| Os05g0370650 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os05g0392050 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os05g0395400 |  | Hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os05g0405400 |  | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os05g0407100 |  | Four F5 protein family protein | | | 35 | 35.2 | | Unknown |
| Os05g0433100 |  | Similar to Serine/threonine-protein kinase SAPK4 | | | 29 | 29.4 | | Protein.postranslational modification |
| Os05g0437401 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os05g0438500 |  |  | 23.4.99 |
| Os05g0440150 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os05g0456925 |  | Similar to regulator of chromosome condensation (RCC1) family protein | | | 31 | 31.2 | | Cell division |
| Os05g0460000 | OsctHSP70-1 | Similar to 70 kDa heat shock cognate protein 1 | | | 20 | 20.2.1 | | Stress |
| Os05g0474600 |  | Similar to Aldose reductase-related protein (EC 1.1.1.21) | | | 33 | 33.99 | | Development.unspecified |
| Os05g0517400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os05g0519000 | OsVQ21 | VQ domain containing protein | | | 35 | 35.2 | | Unknown |
| Os05g0519700 | HSP101 | Heat shock protein%2C Long-term acquired thermotoleranc | | | 20 | 20.2.1 | | Stress |
| Os05g0535800 |  | Similar to F14O23.10 protein | | | 29 | 29.2.1.1.3.1.1 | | Protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S1 |
| Os05g0561600 |  | Protein of unknown function DUF1421 domain containing protein | | | 10 | 10.5.4 | | Cell wall.cell wall proteins.HRGP |
| Os05g0570000 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os05g0595100 | OsUGE1 | Uridine-diphospho-(UDP)-glucose 4-epimerase%2C Cell wall carbohydrate partitioning during nitrogen (N) limitatio | | | 10 | 10.1.2 | | Cell wall.precursor synthesis.UGE |
| Os06g0102725 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os06g0107700 | OsLFNR2 |  | 1.1.5.3 |
| Os06g0110200 | OsLEA2 | Late embryogenesis abundant (LEA) group 1 family protein | | | 33 | 33.2 | | Development.late embryogenesis abundant |
| Os06g0131001 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os06g0133400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0141600 | OsENOD93 | Early nodulin 93 ENOD93 protein family protein | | | 35 | 35.2 | | Unknown |
| Os06g0142200 | OSENOD93A | Early nodulin | | | 35 | 35.2 | | Unknown |
| Os06g0142350 | UDP-GT | Similar to Early nodulin | | | 35 | 35.2 | | Unknown |
| Os06g0142400 | OsENOD93 | Early nodulin | | | 35 | 35.2 | | Unknown |
| Os06g0147100 |  | Similar to cDNA clone:J023088C01%2C full insert sequence | | | 35 | 35.2 | | Unknown |
| Os06g0147500 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os06g0157125 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os06g0160200 | OsGELP80 | Similar to Lanatoside 15'-O-acetylesterase precursor | | | 26 | 26.28 | | Misc.GDSL-motif lipase |
| Os06g0167125 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os06g0169800 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os06g0181100 |  | Octicosapeptide/Phox/Bem1p domain containing protein | | | 35 | 35 | | Unknown |
| Os06g0184766 |  | Hypothetical conserved gene | | | 34 | 34.16 | | Transport.ABC transporters and multidrug resistance systems |
| Os06g0192676 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os06g0197550 |  | Similar to Chaperonin | | | 20 | 20.2 | | Stress.abiotic |
| Os06g0197575 |  | Similar to Chaperonin | | | 29 | 29.6 | | Protein.folding |
| Os06g0219900 |  | Similar to Phi-1 protein | | | 30 | 30.1.1 | | Signalling.in sugar and nutrient physiology |
| Os06g0220100 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os06g0220900 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0223900 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os06g0255200 |  | Conserved hypothetical protein | | | 28 | 28.1 | | DNA.synthesis/chromatin structure |
| Os06g0259901 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os06g0261300 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0264700 |  | Acylphosphatase domain containing protein | | | 35 | 35.2 | | Unknown |
| Os06g0313000 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os06g0330250 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os06g0340001 |  | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os06g0505202 |  | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os06g0506850 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os06g0513050 | OsTHI3 | Conserved hypothetical protein | | | 20 | 20.1 | | Stress.biotic |
| Os06g0513943 | OsTHI6 | Conserved hypothetical protein | | | 20 | 20.1 | | Stress.biotic |
| Os06g0514100 | Osthi7 | Conserved hypothetical protein | | | 20 | 20.1 | | Stress.biotic |
| Os06g0523300 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0558766 |  | Similar to predicted protein | | | 27 | 27.1 | | RNA.processing |
| Os06g0559400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0566201 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os06g0573600 | OsBgal2 | Similar to Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) | | | 26 | 26.3.2 | | Misc.gluco-, galacto- and mannosidases.beta-galactosidase |
| Os06g0582400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0611100 |  | Similar to IQ calmodulin-binding motif family protein | | | 35 | 35 | | Unknown |
| Os06g0611300 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0614400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0622550 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os06g0639550 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os06g0643750 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os06g0664300 |  | Similar to Vacuolar sorting receptor 6 precursor (AtVSR6) (Epidermal growth factor receptor-like protein 6) (AtELP6) (BP80-like protein d) (AtBP80d) | | | 29 | 29.3.4.3 | | Protein.targeting.secretory pathway.vacuole |
| Os06g0694200 | OsGELP88 | Esterase%2C SGNH hydrolase-type domain containing protein | | | 26 | 26.28 | | Misc.GDSL-motif lipase |
| Os06g0716750 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os06g0717850 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os06g0728902 | OsGSL6 | Similar to predicted protein | | | 3 | 3.6 | | Minor CHO metabolism |
| Os07g0100800 | OsProT3 | Similar to Amino acid permease | | | 34 | 34.3 | | Transport.amino acids |
| Os07g0107300 |  | Plant disease resistance response protein family protein | | | 20 | 20.1.7 | | Stress.biotic.PR-proteins |
| Os07g0119800 |  | Protein of unknown function DUF538 domain containing protein | | | 35 | 35.2 | | Unknown |
| Os07g0136866 |  | Similar to BRI1-KD interacting protein 133 (Fragment) | | | 35 | 35 | | Unknown |
| Os07g0155600 | EIN2 | Nramp ion-transporter family protein%2C Ethylene signaling pathwa | | | 34 | 34.12 | | Transport.metal |
| Os07g0176400 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os07g0179700 |  | Hypothetical conserved gene | | | 29 | 29.5 | | Protein.degradation |
| Os07g0184850 |  | Similar to histone H1 | | | 35 | 35 | | Unknown |
| Os07g0203275 |  | Ribosomal protein S1%2C RNA-binding domain domain containing protein | | | 29 | 29.2.1 | | Protein.synthesis\_ribosomal protein |
| Os07g0204400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os07g0206400 | pro13a.1 | 13 kDa prolamin precursor | | | 33 | 33.1 | | Development.storage proteins |
| Os07g0206500 | pro13a.2 | 13 kDa prolamin precursor | | | 33 | 33.1 | | Development.storage proteins |
| Os07g0212400 |  | Transposase%2C Ptta/En/Spm%2C plant domain containing protein | | | 4 | 4.1.6 | | Protein.postranslational modification.kinase.receptor like cytoplasmatic kinase X |
| Os07g0219250 | pro13b.1 | Similar to cDNA%2C clone: J090058L24%2C full insert sequence | | | 33 | 33.1 | | Development.storage proteins |
| Os07g0219400 | pro13b.3 | Prolamin precursor | | | 33 | 33.1 | | Development.storage proteins |
| Os07g0226200 |  | Hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os07g0243150 |  | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os07g0277200 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os07g0413800 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os07g0419300 |  | Similar to Thaumatin-like protein | | | 20 | 20.1 | | Stress.biotic |
| Os07g0448400 | OsPIP2 | Similar to Aquaporin PIP2-5 | | | 34 | 34.19.1 | | Transport.Major Intrinsic Proteins.PIP |
| Os07g0451101 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os07g0453132 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os07g0504200 |  | Hypothetical conserved gene | | | 27 | 27.2 | | RNA.transcription |
| Os07g0509800 | OsAPRL1 | Similar to adenosine 5'-phosphosulfate reductase 2 | | | 14 | 14.2 | | S-assimilation.APR |
| Os07g0523400 | OsGPT2-3 | Glucose-6-phosphate/phosphate-translocator precursor | | | 34 | 34.8 | | Transport.metabolite transporters at the envelope membrane |
| Os07g0523600 | OsGPT2 | Similar to Glucose-6-phosphate/phosphate-translocator precursor | | | 34 | 34.8 | | Transport.metabolite transporters at the envelope membrane |
| Os07g0523965 |  | Similar to Glucose-6-phosphate/phosphate-translocator precursor | | | 34 | 34.8 | | Transport.metabolite transporters at the envelope membrane |
| Os07g0524200 |  | Harpin-induced 1 domain containing protein | | | 33 | 33.2 | | Development.late embryogenesis abundant |
| Os07g0529600 | OsDR8 | Similar to Thiazole biosynthetic enzyme 1-1%2C chloroplast precursor | | | 18 | 18.2 | | Co-factor and vitamine metabolism.thiamine |
| Os07g0546050 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os07g0553700 |  | Similar to Light induced protein like | | | 35 | 35.2 | | Unknown |
| Os07g0564750 |  | Conserved hypothetical protein | | | 30 | 30.5 | | Signalling.G-proteins |
| Os07g0567500 |  | Similar to predicted protein | | | 35 | 35.2 | | Unknown |
| Os07g0587450 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os07g0595750 |  | Similar to predicted protein | | | 35 | 35 | | Unknown |
| Os07g0599900 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os07g0609100 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os07g0624700 |  | UMP/CMP kinase a (EC 2.7.1.48) | | | 23 | 23.4.3 | | Nucleotide metabolism.phosphotransfer and pyrophosphatases.uridylate kinase |
| Os07g0633200 |  | Similar to SC35-like splicing factor SCL30a%2C 30a kD | | | 27 | 27.1.1 | | RNA.processing.splicing |
| Os07g0634400 |  | HAD-superfamily hydrolase%2C subfamily IA%2C variant 3 domain containing protein | | | 35 | 35.2 | | Unknown |
| Os07g0647550 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os07g0675200 | OsEnS-114 | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os07g0679050 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os07g0684000 |  | Ricin B-related lectin domain containing protein | | | 33 | 33 | | Development |
| Os08g0104400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os08g0104900 |  | Protein of unknown function DUF6%2C transmembrane domain containing protein | | | 34 | 34.8 | | Transport.metabolite transporters at the envelope membrane |
| Os08g0106501 |  | Protein of unknown function DUF679 family protein | | | 35 | 35.2 | | Unknown |
| Os08g0106700 |  | Similar to 10A19I.15 | | | 35 | 35 | | Unknown |
| Os08g0109300 | AK1 | Homolog of Arabidopsis ADENOSINE MONOPHOSPHATE KINASE 2 (AMK2)%2C A member of adenylate kinase (AK) famil | | | 23 | 23.4.1 | | Nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate kinase |
| Os08g0112700 | MADS26 | MADS-box transcription factor%2C Regulator of both biotic and abiotic stress response | | | 27 | 27.3.24 | | RNA.regulation of transcription.MADS box transcription factor family |
| Os08g0157600 | CCA1 | MYB transcription factor%2C Circadian cloc | | | 27 | 27.3.26 | | RNA.regulation of transcription.MYB-related transcription factor family |
| Os08g0184700 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os08g0207500 | OsZIP4 | Similar to Zinc transporter ZIP1 (Fragment) | | | 34 | 34.12 | | Transport.metal |
| Os08g0237500 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os08g0243866 |  | Similar to chromatin remodeling complex subunit | | | 27 | 27.3.44 | | RNA.regulation of transcription.Chromatin Remodeling Factors |
| Os08g0269000 |  | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os08g0300501 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os08g0374000 | OsBetvI | Bet v I allergen family protein | | | 8 | 8.3 | | TCA / org. transformation |
| Os08g0377500 |  | Protein of unknown function DUF599 family protein | | | 35 | 35.2 | | Unknown |
| Os08g0382400 | OsCYP38 | Peptidyl-prolyl cis-trans isomerase%2C cyclophilin-type domain containing protein | | | 29 | 29.6 | | Protein.folding |
| Os08g0383750 |  | Hypothetical genes | | | 35 | 35 | | Unknown |
| Os08g0386125 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os08g0413500 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os08g0414900 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os08g0415400 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os08g0431800 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os08g0433050 |  | Similar to Arginine decarboxylase | | | 35 | 35.2 | | Unknown |
| Os08g0459333 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os08g0472800 | OsABA8OX2 | Cytochrome P450 family protein | | | 26 | 26.1 | | Misc.misc2 |
| Os08g0499250 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os08g0500400 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os08g0502000 |  | Conserved hypothetical protein | | | 27 | 27.3.67 | | RNA.regulation of transcription.putative transcription regulator |
| Os08g0508500 | JMJ717 | Similar to predicted protein | | | 27 | 27.3.57 | | RNA.regulation of transcription.JUMONJI family |
| Os08g0518800 | OsGH | Similar to Class III chitinase homologu | | | 20 | 20.1 | | Stress.biotic |
| Os08g0531000 | NPP1 | Nucleotide pyrophosphatase/phosphodiesterase%2C Negative effect on plant growth and starch accumulatio | | | 26 | 26.13 | | Misc.acid and other phosphatases |
| Os08g0532350 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os08g0536300 | OsBBX26 | Similar to Hd1 | | | 27 | 27.3.7 | | RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family |
| Os08g0546800 | HSFB2B | Similar to Heat stress transcription factor B-2b | | | 27 | 27.3.23 | | RNA.regulation of transcription.HSF,Heat-shock transcription factor family |
| Os08g0557800 |  | Similar to Fatty acyl coA reductase | | | 11 | 11.9.4.13 | | Lipid metabolism.lipid degradation.beta-oxidation.acyl CoA reductase |
| Os09g0252700 |  | Similar to E3 ubiquitin protein ligase UPL1 (EC 6.3.2.-) (Ubiquitin-protein ligase 1) | | | 29 | 29.5 | | Protein.degradation |
| Os09g0261400 |  | Protein of unknown function DUF1296 family protein | | | 35 | 35.2 | | Unknown |
| Os09g0294000 |  | Similar to Bifunctional aspartokinase/homoserine dehydrogenase 2%2C chloroplast precursor (AK-HD 2) (AK-HSDH 2) [Includes: Aspartokinase (EC 2.7.2.4)%3B Homoserine dehydrogenase (EC 1.1.1.3)] | | | 13 | 13.1.3.6.1.1 | | Amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspartate kinase |
| Os09g0294300 | OsUBC40 | Ubiquitin-conjugating enzyme/RWD-like domain containing protein | | | 29 | 29.5.11.3 | | Protein.degradation.ubiquitin.E2 |
| Os09g0321000 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os09g0322000 |  | Similar to PaMst-1 | | | 35 | 35.2 | | Unknown |
| Os09g0327000 |  | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os09g0331900 |  | Hypothetical conserved gene | | | 35 | 35.2 | | Unknown |
| Os09g0346500 | CAB1R | Similar to Chlorophyll a-b binding protein%2C chloroplast precursor (LHCII type I CAB) (LHCP) | | | 1 | 1.1.1.1 | | Photosyntheisis |
| Os09g0364400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os09g0391501 |  | Hypothetical gene | | | 35 | 35.2 | | Unknown |
| Os09g0397800 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os09g0401600 |  | Similar to PUX2 (PLANT UBX DOMAIN-CONTAINING PROTEIN 2)%3B nucleic acid binding / zinc ion binding | | | 27 | 27.3.99 | | RNA.regulation of transcription.unclassified |
| Os09g0412300 |  | Similar to Calmodulin-like protein | | | 35 | 35.2 | | Unknown |
| Os09g0417600 | WRKY76 | WRKY transcription factor%2C Transcriptional repressor%2C Pathogen defens | | | 27 | 27.3.32 | | RNA.regulation of transcription.WRKY domain transcription factor family |
| Os09g0425500 |  | Hypothetical gene | | | 35 | 35.2 | | Unknown |
| Os09g0437500 |  | Dormancyauxin associated family protein | | | 35 | 35.2 | | Unknown |
| Os09g0444500 | OsBRXL5 | Similar to Protein Brevis radix-like 1 | | | 20 | 20 | | Stress |
| Os09g0458700 |  | EF hand domain containing protein | | | 35 | 35.2 | | Unknown |
| Os09g0512700 | NEF | Armadillo-like helical domain containing protein | | | 34 | 34 | | Transport |
| Os09g0514500 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os09g0514550 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os09g0515550 |  | Hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os09g0522000 | OsDREB1B | Similar to Dehydration-responsive element-binding protein 1B | | | 17 | 17.5.2 | | Hormone metabolism.ethylene.signal transduction |
| Os09g0526600 | HSFB2C | Similar to Isoform 2 of Heat stress transcription factor B-2c | | | 27 | 27.3.23 | | RNA.regulation of transcription.HSF,Heat-shock transcription factor family |
| Os09g0528200 | Oshox6 | Similar to Homeobox-leucine zipper protein HOX6 | | | 27 | 27.3.22 | | RNA.regulation of transcription.HB,Homeobox transcription factor family |
| Os09g0538000 | OsRNS5 | Ribonuclease T2 family protein | | | 27 | 27.1.19 | | RNA.processing.ribonucleases |
| Os09g0552900 | ONAC110 | Similar to NAC domain protein%2C IPR003441 | | | 33 | 33.99 | | Development.unspecified |
| Os09g0554101 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os09g0558050 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os10g0154566 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os10g0156200 |  | Similar to Protein kinase domain containing protein | | | 29 | 29.4 | | Protein.postranslational modification |
| Os10g0195250 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os10g0325400 | OsREM0.2 | Remorin%2C C-terminal domain containing protein | | | 33 | 33 | | Development |
| Os10g0340450 |  | Similar to Putative defensin-like protein 134 | | | 35 | 35.2 | | Unknown |
| Os10g0364900 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os10g0388701 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os10g0389500 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os10g0390550 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os10g0392600 | OsSPX3 | SPX domain-containing protein%2C Negative regulation of phosphate signaling%2C Pi homeostasi | | | 20 | 20.2 | | Stress.abiotic |
| Os10g0450900 | GRP | Similar to Glycine-rich cell wall structural protein 2 precursor | | | 10 | 10 | | Cell wall |
| Os10g0452500 |  | Similar to Glycine-rich protein precursor | | | 35 | 35.2 | | Unknown |
| Os10g0456800 | DCA1 | CHY zinc finger protein%2C Transcriptional co-activator of DST (Drought and Salt Tolerance: zinc finger transcription factor gene)%2C Drought and salt tolerance%2C Stomatal aperture contro | | | 29 | 29.5.11.4.2 | | Protein.degradation.ubiquitin.E3.RING |
| Os10g0472400 |  | Similar to Thioredoxin | | | 35 | 35.2 | | Unknown |
| Os10g0489000 |  | Similar to FIP1 | | | 17 | 17.1.3 | | Hormone metabolism.abscisic acid.induced-regulated-responsive-activated |
| Os10g0509600 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os10g0511800 |  | Similar to Plus-3 domain containing protein%2C expressed | | | 35 | 35 | | Unknown |
| Os10g0544933 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os10g0550066 | OsMED12\_2 | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os10g0550400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os10g0562000 |  | Similar to glycoprotein | | | 35 | 35.2 | | Unknown |
| Os10g0565401 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os10g0579150 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os11g0111900 |  | BTB domain containing protein | | | 29 | 29.5.11.4.5.2 | | Protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ |
| Os11g0133700 |  | Similar to Glucosamine-fructose-6-phosphate aminotransferase%2C isomerizing family protein%2C expressed | | | 3 | 3.5 | | Minor CHO metabolism |
| Os11g0138600 |  | Similar to Phosphoglycerate mutase family protein | | | 4 | 4.3.12 | | Glycolysis |
| Os11g0151700 | OsPAP21b | Purple acid phosphatase (EC:3.1.3.2)%2C Improvement in phosphate acquisition and utilizatio | | | 26 | 26.13 | | Misc.acid and other phosphatases |
| Os11g0151800 | OsPAP20a | Similar to ATPAP18/PAP18 | | | 26 | 26.13 | | Misc.acid and other phosphatases |
| Os11g0153100 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os11g0168250 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os11g0172133 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os11g0195800 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os11g0210500 | Adh2\* | Similar to Alcohol dehydrogenase | | | 26 | 26.11.1 | | Misc.alcohol dehydrogenases |
| Os11g0235400 |  | Hypothetical genes | | | 35 | 35 | | Unknown |
| Os11g0244200 |  | Similar to Pisum sativum 17.9 kDa heat shock protein (hsp17.9) (Fragment) | | | 20 | 20.2 | | Stress.abiotic |
| Os11g0249800 |  | Non-protein coding transcript | | | 35 | 35 | | Unknown |
| Os11g0434800 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os11g0447300 | OsRALF-1 | GTP-binding protein%2C HSR1-related domain containing protein | | | 30 | 30.5 | | Signalling.G-proteins |
| Os11g0474100 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os11g0496500 |  | Similar to AT.I.24-5 protein (Fragment) | | | 35 | 35.2 | | Unknown |
| Os11g0518600 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os11g0546500 | OsGT6 | Galactosyl transferase family protein | | | 26 | 26.2 | | Misc.UDP glucosyl and glucoronyl transferases |
| Os11g0547000 | FKF1 | Autonomous floral activator%2C Promotion of flowerin | | | 29 | 29.5.11.4.3.2 | | Protein.degradation.ubiquitin.E3.SCF.FBOX |
| Os11g0595200 |  | PAP fibrillin family protein | | | 31 | 31.1 | | Cell organisation |
| Os11g0620150 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os11g0621200 |  | Similar to OSIGBa0117N13.1 protein | | | 13 | 13 | | Amino acid metabolism |
| Os11g0629100 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os11g0641300 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os11g0707000 | OsRcaII | Similar to Ribulose bisphosphate carboxylase/oxygenase activase%2C chloroplastic | | | 1 | 1.3.13 | | Photosyntheisis |
| Os11g0709000 |  | Similar to H0124E07.4 protein | | | 35 | 35 | | Unknown |
| Os12g0104766 |  | Similar to Clathrin heavy chain | | | 31 | 31 | | Cell organisation |
| Os12g0108500 | OsFbox636 | Similar to Leucine Rich Repeat family protein%2C expressed | | | 29 | 29.5.11.4.3.2 | | Protein.degradation.ubiquitin.E3.SCF.FBOX |
| Os12g0111500 |  | BTB domain containing protein | | | 29 | 29.5.11.4.5.2 | | Protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ |
| Os12g0112251 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os12g0112500 | OsPP124 | Protein-tyrosine phosphatase%2C dual specificity domain containing protein | | | 2 | 2.2.2.10 | | major CHO metabolism |
| Os12g0114100 | OsWNK8 | Similar to MAP kinase-like protein | | | 29 | 29.4 | | Protein.postranslational modification |
| Os12g0135100 |  | Similar to Phosphoglycerate mutase family protein | | | 4 | 4.3.12 | | Glycolysis |
| Os12g0139400 | RR10 | A-type response regulator%2C Cytokinin signalin | | | 27 | 27.3.5 | | RNA.regulation of transcription.ARR |
| Os12g0151000 | OsPAP20b | Similar to Purple acid phosphatase | | | 26 | 26.13 | | Misc.acid and other phosphatases |
| Os12g0156000 | OsS40-11 | Similar to OSIGBa0134P10.11 protein | | | 35 | 35.2 | | Unknown |
| Os12g0183100 |  | Similar to Branched chain alpha-keto acid dehydrogenase E1-alpha subunit (Fragment) | | | 35 | 35 | | Unknown |
| Os12g0189300 |  | Pyruvate/Phosphoenolpyruvate kinase%2C catalytic core domain containing protein | | | 27 | 27.3.99 | | RNA.regulation of transcription.unclassified |
| Os12g0204550 |  | Hypothetical gene | | | 35 | 35 | | Unknown |
| Os12g0210601 |  | Hypothetical conserved gene | | | 35 | 35 | | Unknown |
| Os12g0226400 |  | Similar to 2-alkenal reductase | | | 26 | 26.7 | | Misc.oxidases - copper, flavone etc. |
| Os12g0244150 |  | Hypothetical protein | | | 35 | 35 | | Unknown |
| Os12g0269100 | pro13a.3 | Similar to Prolamin | | | 33 | 33.1 | | Development.storage proteins |
| Os12g0274700 | RBCS | Similar to Petunia ribulose 1%2C5-bisphosphate carboxylase small subunit mRNA (clone pSSU 51)%2C partial cds. (Fragment) | | | 1 | 1.3.2 | | Photosyntheisis |
| Os12g0288801 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os12g0291100 | RbcS3 | Similar to Petunia ribulose 1%2C5-bisphosphate carboxylase small subunit mRNA (clone pSSU 51)%2C partial cds. (Fragment) | | | 16 | 16.2 | | Secondary metabolism.phenylpropanoids |
| Os12g0493900 |  | Armadillo-like helical domain containing protein | | | 35 | 35.2 | | Unknown |
| Os12g0548401 |  | Similar to Proteinase inhibitor | | | 35 | 35.2 | | Unknown |
| Os12g0548700 |  | Similar to MPI | | | 35 | 35.2 | | Unknown |
| Os12g0575300 |  | Conserved hypothetical protein | | | 35 | 35 | | Unknown |
| Os12g0575400 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os12g0576100 |  | Conserved hypothetical protein | | | 35 | 35.2 | | Unknown |
| Os12g0583700 | RZF71 | Zinc finger%2C C2H2-type domain containing protein | | | 27 | 27.3.11 | | RNA.regulation of transcription.C2H2 zinc finger family |
| Os12g0586100 | SAPK9 | Serine/threonine protein kinase%2C Abscisic acid (ABA)-activated protein kinase%2C Hyperosmotic stress response%2C ABA signal transductio | | | 29 | 29.4 | | Protein.postranslational modification |
| Os12g0610600 | OMTN3 | NAC transcription factor%2C Negative regulation of drought toleranc | | | 33 | 33.99 | | Development.unspecified |
| Os12g0630600 |  | Carbohydrate/puine kinase%2C PfkB%2C conserved site containing protein | | | 29 | 29.2.1 | | Protein.synthesis\_ribosomal protein |